

FIGURE 1

Target segment starts with AA

Target segment: 5' -> 3'

	GC Ratio	Position	siRNA Sense strand: 5' -> 3' siRNA Antisense strand: 3' -> 5'
AATGTCCACATGTCAGGAGGC [SEQ ID NO:11]	0.52	93	UGUCCACAUUGUCAGGAGGCUU [SEQ ID NO:29] UUACAGGUGUACAGUCCUCCG [SEQ ID NO:47]
AACAAGACTGGACCATCCAGT [SEQ ID NO:12]	0.48	124	CAAGACUGGACCAUCCAGUUU [SEQ ID NO:30] UUGUUCUGACCUGGUAGGUCA [SEQ ID NO:48]
AAGTGCCTCCAGCACTATTGT [SEQ ID NO:13]	0.48	246	GUGCGUCCAGCACUAUUGUUU [SEQ ID NO:31] UUCACGCAGGUCGUGAUAAACA [SEQ ID NO:49]
AACCTCAAGATCCACAGCAGC [SEQ ID NO:14]	0.52	648	CCUCAAGAUCCACAGCAGCUU [SEQ ID NO:32] UUGGAGUUCUAGGUGUCGUCG [SEQ ID NO:50]
AAGTACTGGATGTCTCAGACG [SEQ ID NO:15]	0.48	888	GUACUGGAUGUCUCAGACGUU [SEQ ID NO:33] UUCAUGACCUACAGAGUCUGC [SEQ ID NO:51]
AAGGTTAGTCCGGACAGAGTC [SEQ ID NO:16]	0.52	1037	GGUUAGUCCGGACAGAGUCUU [SEQ ID NO:34] UUCCAAUCAGGCCUGUCUCAG [SEQ ID NO:52]
AAGCCACCTCGCTATTCAGAC [SEQ ID NO:17]	0.52	1089	GCCACCUCGCUAUUCAGACUU [SEQ ID NO:35] UUCGGUGGAGCGAUAGUCUG [SEQ ID NO:53]
AAGAACTTCAACCTGCCAGCA [SEQ ID NO:18]	0.48	1305	GAACUUCAACCUGCCAGCAUU [SEQ ID NO:36] UUCUUGAAGUUGGACGGUCGU [SEQ ID NO:54]
AACTTCAACCTGCCAGCATCC [SEQ ID NO:19]	0.52	1308	CUUCAACCUGCCAGCAUCCUU [SEQ ID NO:37] UUGAAGUUGGACGGUCGUAGG [SEQ ID NO:55]

AATTGAAGTGGAGCCAACGTC [SEQ ID NO:20]	0.48	1463	UUGAAGUGGAGCCAACGUCUU [SEQ ID NO:38] UUAACUUCACCUCGGUUGCAG [SEQ ID NO:56]
AACGTCGGAGAATGAAGAGGT [SEQ ID NO:21]	0.48	1478	CGUCGGAGAAUGAAGAGGUUU [SEQ ID NO:39] UUGCAGCCUCUACUUUCUCCA [SEQ ID NO:57]
AAGAGTCAGAGGATGACTTCG [SEQ ID NO:22]	0.48	1513	GAGUCAGAGGAUGACUUCGUU [SEQ ID NO:40] UUCUCAGUCUCCUACUGAAGC [SEQ ID NO:58]
AACCAGGCAGATTGCTCAAGA [SEQ ID NO:23]	0.48	1922	CCAGGCAGAUUGCUCAGAUU [SEQ ID NO:41] UUGGUCCGUCUAACGAGUUCU [SEQ ID NO:59]
AACGTCTTCTATGACAACGGC [SEQ ID NO:24]	0.48	2007	CGUCUUCUAUGACAACGGCUU [SEQ ID NO:42] UUGCAGAAGAUACUGUUGCCG [SEQ ID NO:60]
AACTGCGCATCCAGAATGGCT [SEQ ID NO:25]	0.52	2098	CUGCGCAUCCAGAAUGGUUU [SEQ ID NO:43] UUGACCGUAGGUUCUACCGA [SEQ ID NO:61]
AATCTGGTATGAACCTCACGC [SEQ ID NO:26]	0.48	2222	UCUGGUUAUGAACUCCACGCCU [SEQ ID NO:44] UUAGACCAUACUUGAGGUGCG [SEQ ID NO:62]
AACCTCAGCCAGATTGGCATG [SEQ ID NO:27]	0.52	2313	CCUCAGCCAGAUUGGCAUGUU [SEQ ID NO:45] UUGGAGUCGGUCUAACCGUAC [SEQ ID NO:63]
AAGAGAGACCTACCTCACCA [SEQ ID NO:28]	0.48	2383	GAGAGACCUACCUUCACCAUU [SEQ ID NO:46] UUCUCUCUGGAUGGAAGUGGU [SEQ ID NO:64]

Target segment starts with CA

Target segment: 5' -> 3'

GC Ratio Position siRNA Sense strand: 5' -> 3'
siRNA Antisense strand: 3' -> 5'

CAGGAATGTCCACATGTCAGG [SEQ ID NO:65]	0.52	89	GGAAUGUCCACAUUGUCAGGUU [SEQ ID NO:94] UUCCUUACAGGUGUACAGUCC [SEQ ID NO:123]
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CACATGTCAGGAGGCAACCTT [SEQ ID NO:66]	0.52	99	CAUGUCAGGAGGCAACCUUU [SEQ ID NO:95] UUGUACAGUCGUCCGUUGGAA [SEQ ID NO:124]
CAAGTGCCTCCAGCACTATTG [SEQ ID NO:67]	0.52	245	AGUGCGUCCAGCACUAUUGUU [SEQ ID NO:96] UUUCACGCAGGUCGUGAUAC [SEQ ID NO:125]
CAGCACTATTGTCACACCAGC [SEQ ID NO:68]	0.52	255	GCACUAUUGUCACACCAGCUU [SEQ ID NO:97] UUCGUGAUACAGUGUGGUCG [SEQ ID NO:126]
CACACTGAGGCCAACCTCTCT [SEQ ID NO:69]	0.52	783	CACUGAGGCCAACUUCUCUUU [SEQ ID NO:98] UUGUGACUCCGGUUGAAGAGA [SEQ ID NO:127]
CAGAGATCTCGGCAACTCCAT [SEQ ID NO:70]	0.52	848	GAGAUCUCGGCAACUCCAUUU [SEQ ID NO:99] UUCUCUAGAGCCGUUGAGGUA [SEQ ID NO:128]
CAACTCCATCAAGCACAGGTT [SEQ ID NO:71]	0.48	860	ACUCCAUCAGCACAGGUUUU [SEQ ID NO:100] UUUGAGGUAGUUCGUGUCCAA [SEQ ID NO:129]
CACCAAGTACTGGATGTCTCA [SEQ ID NO:72]	0.48	884	CCAAGUACUGGAUGUCUCAUU [SEQ ID NO:101] UUGGUUCAUGACCUACAGAGU [SEQ ID NO:130]
CAAGTACTGGATGTCTCAGAC [SEQ ID NO:73]	0.48	887	AGUACUGGAUGUCUCAGACUU [SEQ ID NO:102] UUUCAUGACCUACAGAGUCUG [SEQ ID NO:131]
CATCTCTGATCATCCACCGA [SEQ ID NO:74]	0.48	1005	UCUUCUGAUCAUCCACCGAUU [SEQ ID NO:103] UUAGAAGACUAGUAGGUGGCU [SEQ ID NO:132]
CAAGGTTAGTCCGGACAGAGT [SEQ ID NO:75]	0.52	1036	AGGUUAGUCCGGACAGAGUUU [SEQ ID NO:104] UUUCCAAUCAGGCCUGUCUCA [SEQ ID NO:133]
CAGACCTGCACATCAGTCAGA [SEQ ID NO:76]	0.52	1105	GACCUGCACAUCAUCAGUCAGAUU [SEQ ID NO:105] UUCUGGACGUGUAGUCAGUCU [SEQ ID NO:134]

CACACGGCAGCAGAAGAACCTT [SEQ ID NO:77]	0.52	1292	CACGGCAGCAGAAGAACUUUU [SEQ ID NO:106] UUGUGCCGUCGUUCUUGAA [SEQ ID NO:135]
CACGGCAGCAGAAGAACTTCA [SEQ ID NO:78]	0.52	1294	CGGCAGCAGAAGAACUUCAUU [SEQ ID NO:107] UUGCCGUCGUUCUUGAAGU [SEQ ID NO:136]
CAGCAGAAGAACCTCAACCTG [SEQ ID NO:79]	0.48	1299	GCAGAAGAACUUCAACCUGUU [SEQ ID NO:108] UUCGUCUUCUUGAAGUUGGAC [SEQ ID NO:137]
CAGAAGAACTTCAACCTGCCA [SEQ ID NO:80]	0.48	1302	GAAGAACUUCAACCUGCCAUU [SEQ ID NO:109] UUCUUCUUGAAGUUGGACGGU [SEQ ID NO:138]
CAACGTCGGAGAATGAAGAGGG [SEQ ID NO:81]	0.52	1477	ACGUCCGGAGAAUGAAGAGGUU [SEQ ID NO:110] UUUGCAGCCUCUUACUUCUCC [SEQ ID NO:139]
CATGATGAGGCCGAAGAGTCA [SEQ ID NO:82]	0.52	1500	UGAUGAGGCCGAAGAGUCAUU [SEQ ID NO:111] UUACUACUCCGGCUUCUCAGU [SEQ ID NO:140]
CAGAGGATGACTCGAGGAGA [SEQ ID NO:83]	0.52	1519	GAGGAUGACUUUCGAGGAGAUU [SEQ ID NO:112] UUCUCCUACUGAAGCUCCUCU [SEQ ID NO:141]
CAGACCAGCATTTCTTCAG [SEQ ID NO:84]	0.52	1587	GACCAGCAUCUCCUUCAGUU [SEQ ID NO:113] UUCUGGUCGUAGAAGGAAGUC [SEQ ID NO:142]
CAGCATCTTCCTTCAGGAGTG [SEQ ID NO:85]	0.52	1592	GCAUCUCCUUCAGGAGGUU [SEQ ID NO:114] UUCGUAGAAGGAAGUCCUCAC [SEQ ID NO:143]
CATCCGGCTGATTGACATTGA [SEQ ID NO:86]	0.48	1706	UCCGGCUGAUUGACAUUGAUU [SEQ ID NO:115] UUAGGCCGACUAACUGUAACU [SEQ ID NO:144]
CATCATCACCAAGCCTCTGTAA [SEQ ID NO:87]	0.48	1844	UCAUCACCAGCCUCUGUAUU [SEQ ID NO:116] UUAGUAGUGGUUCGGAGACAUU [SEQ ID NO:145]

CATCCAGAATGGCTGGCTATG [SEQ ID NO:88]	0.52	2105	UCCAGAAUGGCUGGCUAUGUU [SEQ ID NO:117] UUAGGUCUUACCGACCGAUAC [SEQ ID NO:146]
CAATCTGGTATGAACCTCCACG [SEQ ID NO:89]	0.48	2221	AUCUGGUAGAACUCCACGUU [SEQ ID NO:118] UUUAGACCAUACUUGAGGUGC [SEQ ID NO:147]
CAACCAGCAGAGGAATAATC [SEQ ID NO:90]	0.48	2265	ACCAGCAGAGGCAAUAAUCUU [SEQ ID NO:119] UUUGGUCGUCUCCGUUAUUAG [SEQ ID NO:148]
CAGCAGAGGCAATAATCTGGC [SEQ ID NO:91]	0.52	2269	GCAGAGGCAAUAAUCUGGUU [SEQ ID NO:120] UUCGUCUCCGUUAUUAGACCG [SEQ ID NO:149]
CAACCTCAGCCAGATTGGCAT [SEQ ID NO:92]	0.52	2312	ACCUCAGCCAGAUUGGCAUUU [SEQ ID NO:121] UUUGGAGUCGGUCUAACCGUA [SEQ ID NO:150]
CAAGAAGAGAGACCTACCTTC [SEQ ID NO:93]	0.48	2379	AGAAGAGAGACCUACCUUCUU [SEQ ID NO:122] UUUCUUCUCUCUGGAUGGAAAG [SEQ ID NO:151]

Target segment starts with GA

Target segment: 5' -> 3'

	GC Ratio	Position	siRNA Sense strand: 5' -> 3' siRNA Antisense strand: 3' -> 5'
GAATGTCCACATGTCAGGAGG [SEQ ID NO:152]	0.52	92	AUGUCCACAUUGUCAGGAGGUU [SEQ ID NO:181] UUUACAGGUGUACAGUCCUCC [SEQ ID NO:210]
GAAGAAGAACAAAGCTGAAGCC [SEQ ID NO:153]	0.48	476	AGAAGAACAAAGCUGAAGCCUU [SEQ ID NO:182] UUUCUUUCUUGUUCGACUUCGG [SEQ ID NO:211]
GAACCTCAAGATCCACAGCAG [SEQ ID NO:154]	0.52	647	ACCUCAAGAACCCACAGCAGUU [SEQ ID NO:183] UUUGGAGUUCUAGGUGUGUC [SEQ ID NO:212]
GAGATCTGGCAACTCCATCA [SEQ ID NO:155]	0.52	850	GAUCUCGGCAACUCCAUCUU [SEQ ID NO:184] UUCUAGAGCCGUUGAGGUAGU [SEQ ID NO:213]

GATCTCGGCAACTCCATCAAG [SEQ ID NO:156]	0.52	852	UCUCGGCAACUCCAUCAGUU [SEQ ID NO:185] UUAGAGCCGUUGAGGUAGUUC [SEQ ID NO:214]
GATGTCTCAGACGTGCACAGT [SEQ ID NO:157]	0.52	896	UGUCUCAGACGUGCACAGUUU [SEQ ID NO:186] UUACAGAGUCUGCACGUGUCA [SEQ ID NO:215]
GAGGAGATCCAGCAAGGTTAG [SEQ ID NO:158]	0.52	1024	GGAGAUCCAGCAAGGUUAGUU [SEQ ID NO:187] UUCUCUAGGUCGUUCCAAUC [SEQ ID NO:216]
GAGATCCAGCAAGGTTAGTCC [SEQ ID NO:159]	0.52	1027	GAUCCAGCAAGGUUAGUCCUU [SEQ ID NO:188] UUCUAGGUCGUUCCAAUCAGG [SEQ ID NO:217]
GAAGCCACCTCGCTATTCAGA [SEQ ID NO:160]	0.52	1088	AGCCACCUUCGCUAUUCAGAUU [SEQ ID NO:189] UUUCGGUGGAGCGAUAAAGUCU [SEQ ID NO:218]
GAAGAACTTCAACCTGCCAGC [SEQ ID NO:161]	0.52	1304	AGAACUUCAACCUGCCAGCUU [SEQ ID NO:190] UUUCUUGAAGUUGGACGGUCG [SEQ ID NO:219]
GAACTTCAACCTGCCAGCATC [SEQ ID NO:162]	0.52	1307	ACUUCAACCUGCCAGCAUCUU [SEQ ID NO:191] UUUGAAGUUGGACGGUCGUAG [SEQ ID NO:220]
GACCTCGAATCCAATCTTGGA [SEQ ID NO:163]	0.48	1424	CCUCGAAUCCAAUCUUGGAUU [SEQ ID NO:192] UUGGAGCUUAGGUAGAACCU [SEQ ID NO:221]
GAGCCAACGTGGAGAATGAA [SEQ ID NO:164]	0.52	1473	GCCAACGUCGGAGAAUGAAUU [SEQ ID NO:193] UUCGGUUGCAGCCUCUUACUU [SEQ ID NO:222]
GAAGAGTCAGAGGATGACTTC [SEQ ID NO:165]	0.48	1512	AGAGUCAGAGGAUGACUUCUU [SEQ ID NO:194] UUUCUCAGUCUCCUACUGAAG [SEQ ID NO:223]
GAGTCAGAGGATGACTTCGAG [SEQ ID NO:166]	0.52	1515	GUCAGAGGAUGACUUCGAGUU [SEQ ID NO:195] UUCAGUCUCCUACUGAAGCUC [SEQ ID NO:224]

GAGGATGACTTCGAGGAGATG [SEQ ID NO:167]	0.52	1521	GGAUGACUUCGAGGAGAUGUU [SEQ ID NO:196] UUCUACUGAAGCUCCUCUAC [SEQ ID NO:225]
GATGACTTCGAGGAGATGAAC [SEQ ID NO:168]	0.48	1524	UGACUUUCGAGGAGAUGAACUU [SEQ ID NO:197] UUACUGAAGCUCCUCUACUUG [SEQ ID NO:226]
GAATTCGAGGAGATGAACCTG [SEQ ID NO:169]	0.52	1527	CUUCGAGGAGAUGAACCUUU [SEQ ID NO:198] UUGAAGCUCCUCUACUUGGAC [SEQ ID NO:227]
GACCAGCATCTTCCTTCAGGA [SEQ ID NO:170]	0.52	1589	CCAGCAUCUUCUUCAGGAUU [SEQ ID NO:199] UUGGUCGUAGAAGGAAGGUCCU [SEQ ID NO:228]
GACGCTCTATTCCGTTGTGAG [SEQ ID NO:171]	0.52	1871	CGCUCUAUUCGUUGUGAGUU [SEQ ID NO:200] UUGCGAGAUAGGCAACACUC [SEQ ID NO:229]
GAATCCTACACAAGGACCTCA [SEQ ID NO:172]	0.48	1978	AUCCUACACAAGGACCUAUU [SEQ ID NO:201] UUUAGGAUGUGUUCCUGGAGU [SEQ ID NO:230]
GAACGTCTTCTATGACAACGG [SEQ ID NO:173]	0.48	2006	ACGUCUUCUAUGACAACGGUU [SEQ ID NO:202] UUUGCAGAAGAUACUGUUGCC [SEQ ID NO:231]
GACACAGAGGAGGATAAGCTC [SEQ ID NO:174]	0.52	2163	CACAGAGGAGGAAAGCUCUU [SEQ ID NO:203] UUGUGUCUCCUCUAAUCGAG [SEQ ID NO:232]
GACATTCTTCTCTGCTGG [SEQ ID NO:175]	0.48	2349	CAUUCUUCUUCUGCUGGUU [SEQ ID NO:204] UUGUAAGAAGAGAAAGACGACC [SEQ ID NO:233]
GAACAAGAAGAGAGACCTACC [SEQ ID NO:176]	0.48	2376	ACAAGAAGAGAGACCUAUU [SEQ ID NO:205] UUUGUUUCUUCUCUGGAUGG [SEQ ID NO:234]
GAAGAGAGACCTACCTTCACC [SEQ ID NO:177]	0.52	2382	AGAGAGACCUACCUUCACCUU [SEQ ID NO:206] UUUCUCUCUGGAUGGAAGUGG [SEQ ID NO:235]

GAGAGACCTACCTCACCAAG [SEQ ID NO:178]	0.52	2385	GAGACCUACCUUCACCAAGUU [SEQ ID NO:207] UUCUCUGGAUGGAAGUGGUUC [SEQ ID NO:236]
GAGACCTACCTCACCAAGCT [SEQ ID NO:179]	0.52	2387	GACCUACCUUCACCAAGCUUU [SEQ ID NO:208] UUCUGGAUGGAAGUGGUUCGA [SEQ ID NO:237]
GACCTACCTCACCAAGCTCA [SEQ ID NO:180]	0.52	2389	CCUACCUUCACCAAGCUAUU [SEQ ID NO:209] UUGGAUGGAAGUGGUUCGAGU [SEQ ID NO:238]

Target segment starts with TA

Target segment: 5' -> 3'

GC Ratio Position siRNA Sense strand: 5' -> 3'
siRNA Antisense strand: 3' -> 5'

TACTGGATGTCTCAGACGTGC [SEQ ID NO:239]	0.52	891	CUGGAUGUCUCAGACGUGCUU [SEQ ID NO:242] UUGACCUACAGAGUCUGCACG [SEQ ID NO:245]
TACGGAAGCCACCTCGCTATT [SEQ ID NO:240]	0.52	1084	CGGAAGGCCACCUUCGCUAUUUU [SEQ ID NO:243] UUGCCUUCGGUGGGAGCGAUAA [SEQ ID NO:246]
TACCTTCACCAAGCTCATGGA [SEQ ID NO:241]	0.48	2393	CCUUCACCAAGCUAUGGAUU [SEQ ID NO:244] UUGGAAGUGGUUCGAGUACCU [SEQ ID NO:247]

FIGURE 2

CLUSTAL W multiple sequence alignment results

MSF: 1005 Type: P Check: 5073

Name: hksr-1_full_cae84534_1.pep oo Len: 1005 Check: 4093 Weight: 12.1
 Name: mksr-1_np_038599.pep oo Len: 1005 Check: 1555 Weight: 12.7
 Name: hksr-1_partial_aac50354_1.pep oo Len: 1005 Check: 10 Weight: 10.7
 Name: hksr-2_aaq24226_1.pep oo Len: 1005 Check: 732 Weight: 13.8
 Name: mksr-2.pep oo Len: 1005 Check: 2473 Weight: 13.6
 Name: dmksr_np_524236.pep oo Len: 1005 Check: 4070 Weight: 36.8
 Name: ceksr_aaa92436_1.pep oo Len: 1005 Check: 2140 Weight: 26.8

CA1

1	50
hKSR-1(full)	MDRAALRAAA MGEKKEGGGG GDAAAAEGGA GAAASRALQQ CGQLQKLIDI
mKSR-1	MDRAALRAAA MGEKKEGGGG G..AAADGGA GAAVSRALQQ CGQLQKLIDI
hKSR-1(partial)
hKSR-2
mKSR-2
DmKSR MS SNNNAPASAP DTGSTNANDP ISGSLSVDSN LVIIQDMIDL
CeKSR

CA1

51	100
hKSR-1(full)	SIGSLRGLRT KCAVSNDLTQ QEIRTLEAKL VRYICKQRQC KLSVAPGERT
mKSR-1	SIGSLRGLRT KCSVNDLTQ QEIRTLEAKL VKYICKQQQS KLSVTPSDRT
hKSR-1(partial)
hKSR-2 MT DEQVCETVEK YGANREECAR LNALSCLRN VHMSGGNLSK
mKSR-2 MT DEQVCETVEK YGANQEECAR LNALSCLRN VHKGGSNLSK
DmKSR	SANHLEGLRT QCAISSTLTQ QEIRCLESKL VRYFSELLLA KMRLNERIPA
CeKSR

101	150
hKSR-1(full)	PELNSYPRFS DWLYTFNVRP EVV....QEI PRDLTLDALL EMNEAKVKET
mKSR-1	AELNSYPRFS DWLYIFNVRP EVV....QEI PQELTLDALL EMDEAKAKEM
hKSR-1(partial)
hKSR-2	QDWTIQWPTT ETGKENNPVC PPE....PTP WIRTHLSQSP RVPSKCVQHY
mKSR-2	QDWIIQWPTT EPGQESNPVC PPE....PSP WIRTHLSQSP RVQTKCPQHF
DmKSR	NGLVPHTTGN ELRQWLRVVG LSQGTLTACL ARLTTLERQL RLSDEEIRQL
CeKSR

151	200
hKSR-1(full)	LRRCGASGDE CGRL QYALTCLRKV TGLGGEHKED SSWSSLDARR
mKSR-1	LRRWGASTEE CSRL QQALTCLRKV TGLGGEHKMD SGWSSTDARD
hKSR-1(partial)
hKSR-2	CHTSPTPGAP VYTH VDRLTVDAYP GLCPPP.P.LE SGHRSLPPSP
mKSR-2	CPTSPPTPGTP VYTQ VDRLTVDAYP NLCPPPPPLE SGHRSLPPSP
DmKSR	LADSPSQREE EELRRLTRAM QNLRKCMESL ESGTAASNND PEQWHWDSDWD
CeKSR MM QTQVASRAGY SNLPQFGAGI AQDIKTQAIN

CA2

201

250

hKSR-1 (full) ESGSGPSTD T LSAASLPWPP GSSQLGRAGN SAQGPRSI SV SALPASDSPT
 mKSR-1 SSLG..... PPMD MLSSILGRAGA STQGPRSI SV SALPASDSPV
 hKSR-1 (partial)

hKSR-2 RQRHAVRTPP RTPNIVTTVT PPGTPPMRKK NKLKPPGTTP PSSRKLIHLI
 mKSR-2 RQRHVVRTPP RTPNIVTTVT PPGTPPMRKK NKLKPPGTTP PSSRKLIHLI
 DmKSR RPTHIHRGSV GNIGLGNNST ASPRTHHRQH GVKGKNSALA NSTNFKSGRQ
 CeKSR NLKECLKLTT INRFLTSSYE EDAKSVERKI FSAVYQMTKI GLIDREKREI

251

300

hKSR-1 (full) PSFSEGLSDT CIPLHASGRL TPRALHSFIT PPTTPQLRRH TKLKPPRTTP
 mKSR-1 PGLSEGLSDS CIPLHTSGRL TPRALHSFIT PPTTPQLRRH AKLKPPRTTP
 hKSR-1 (partial) .. EFRHTSAL TQHTAHTQHT SAHTQHSFIT PPTTPQLRRH TKLKPPRTTP
 hKSR-2 PGFTALHRSK SHEFQLGHGV DEAHTPKAKK KSKPLNLKIH SSVGSCENIP
 mKSR-2 PGFTALHRSK SHEFQLGNRV DEANTPKAKK KSKPLNLKIH SSVGSCENIP
 DmKSR SPSATEELNS TQGSQTLTLP TPSPPNSPFT PSSGLSSSLN GTPQRSRGTP
 CeKSR NAIWFTFVGL SAQNIRHLEI CSITDFNALF SITNQELRSL ADRGRLDVET

301

350

hKSR-1 (full) PPSRK..... VFQ LLPSFPTLTR SKSHESQLGN
 mKSR-1 PPSRK..... VFQ LLPSFPTLTR SKSHESQLGN
 hKSR-1 (partial) PPSRK..... VFQ LLPSFPTLTR SKSHESQLGN
 hKSR-2 SQQRSP..... LSER SLRSFFVGHA PFLPSTPPVH
 mKSR-2 AQQRSP..... LSER SLRSFFVGHG PFLPSTPPVH
 DmKSR PPARKHQTL SQSHVQVDGE QLARNRLPTD PSPDSHSSTS SDIFVDPNTN
 CeKSR KRKLQLS..... TVILQN HWNAYHSRTS SGSTDPSGQ

CA3

351

400

hKSR-1 (full) RIDDVSSMRF DLHGSPQMV RRDIGLSVTH RFSTKSWLSQ VCHVCQKSMI
 mKSR-1 RIDDVTPMFK ELPHGSPQLV RRDIGLSVTH RFSTKSWLSQ VCNVCQKSMI
 hKSR-1 (partial) RIDDVSSMRF DLHGSPQMV RRDIGLSVTH RFSTKSWLSQ VCHVCQKSMI
 hKSR-2 TEANFSANTL SVPRWSPQIP RRDLGNSIKH RFSTKYWMSQ TCTVCGKGML
 mKSR-2 TEANFSANTL SVPRWSPQIP RRDLGNSIKH RFSTKYWMSQ TCTVCGKGML
 DmKSR ASSGGSSSNV LMVPCSPGVG HVGMGHAIKH RFTKALGFMA TCTLCQKQVF
 CeKSR STPAIVTPSP KFNVPSLSVT SAKMIQSSSM GFATTPKSPK TSSRLVHAIP

CA3

401

450

hKSR-1 (full) FG.VKCKHCR LKCHNKCTKE APACRISFLP ... LTRLRR.
 mKSR-1 FG.VKCKHCR LKCHNKCTKE APACRITFLP ... LARLRR.
 hKSR-1 (partial) FG.VKCKHCR LKCHNKCTKE APACRISFLP ... LTRLRR.
 hKSR-2 FG.LKCKNCK LKCHNKCTKE APPCHLLIIH RGDPARLVR.
 mKSR-2 FG.LKCKNCK LKCHNKCTKE APPCHLLIIH RGDPARLVR.
 DmKSR HRWMKCTDCK YICHKSCAPH VPPSCGLPRE YVDEFRHIKE QGGYASLPHV
 CeKSR HKWHRSTKFR FSGDAVCHFC QRPLGFGFLN AWEKCRSCKW KVHTQCKGRV

CA4

451

500

hKSR-1 (full) ... TESVPSD INNPVDRAAE PHFGTLPKAL TKK..... EH PPAMNHLDSS
 mKSR-1 ... TESVPSD INNPVDRAAE PHFGTLPKAL TKK..... EH PPAMN.LDSS
 hKSR-1 (partial) ... TESVPSD INNPVDRAAE PHFGTLPKAL TKK..... EH PPAMNHLDSS
 hKSR-2 ... TESVPCD INNPLRKPPR YSDLHISQTL PTKTNKINKDH IPVVPYQPDSS
 mKSR-2 ... TESVPCD INNPVRKPAR YSDLHISQTL PTKTNKINKDH IPVVPYQPDSS
 DmKSR HGAAGKSPLV KKSTLKGPLH QQHGDSSSPS SSCTSSTPSS PALFQQRERE
 CeKSR GDSCGLTPDH LRFLFDKLIQ ENNGGMWKDP QSVPGSRSMN EPAFQFPDTA

CA4

501	550
hKSR-1 (full)	SNPSSTTSST PSSPAPFPTS SNPSSATTP.
mKSR-1	SNPSSTTSST PSSPAPFLTS SNPSSATTP.
hKSR-1 (partial)	SNPSSTTSST PSSPAPFPTS SNPSSATTP.
hKSR-2	SNPSSTTSST PSSPAPPLPP SATPPSPLH.
mKSR-2	SNPSSTTSST PSSPAPPLPP SATPPSPLH.
DmKSR	LDQAGSSSSA NLLPTPSLGK HQPSQFNFPN VTVTSSGGSG GVSLISNEPV
CeKSR	IDSSSTNSS APSTPALPAG ISGNVSSLTA PYR. SERK

CA4

551	600
hKSR-1 (full)PNPSPG QRDSRFNFP AYFIHHRQQF IFPDISAFAH AAPLPEAADG
mKSR-1PNPSPG QRDS. RF SFPDISACSQ AAPLSSTADS
hKSR-1 (partial)PNPSPG QRDSRFNFP AYFIHHRQQF IFPDISAFAH AAPLPEAADG
hKSR-2PSPQCT RQQKKNFNLPA SHYYKYKQQF IFPDVVPVPE TPTRAPQVIL
mKSR-2PSPQCP RQKKNFNLPA SHYYKYKQQF IFPDVVPVPE TPTRAPQVIL
DmKSR	PEQFPTAPAT ANGGLDSLVS SSNGHMSSLI GSQTNSASTA ATLTGSLVNS
CeKSR	FLFPDTENYS VHNRLPILVI SEGDHPTTTE IQQETENHNK SAAASMSGNI

601	650
hKSR-1 (full)	TRLDDQPKAD VLEAHEAEAE EPEAGKSEAE DDE. DEVDDL PSSRRPWRG.
mKSR-1	TRLDDQPKTD VLGVHEAEAE EPEAGKSEAE DDEEDEVDDL PSSRRPWRG.
hKSR-1 (partial)	TRLDDQPKAD VLEAHEAEAE EPEAGKSEAE DDE. DEVDDL PSSRRPWRG.
hKSR-2	HPVTSNPILE GNPLLQIEVE PTSENEEVHD EAAESEDDFE EMNLSSAR
mKSR-2	HPVTSNTILE GNPLLQIEVE PTSENEESHN EAAESEDEF EEMNLSSAR
DmKSR	TTTTSTCSFF PRKLSTAGVD KRTPFTSECT DTHKSNDSDK TVSLSGSAST
CeKSR	ESEGTTIVANH EDSTGSQEVD SEAAPSQEAV DKFNKRADGG FTWERHAWN

651	CA5 700
hKSR-1 (full)	PISRKAS.QTSVYLQEW DIPFEQVELG EPIGQGRWGR
mKSR-1	PISRKAS.QTSVYLQEW DIPFEQVELG EPIGQGRWGR
hKSR-1 (partial)	PISRKAS.QTSVYLQEW DIPFEQVELG EPIGQGRWGR
hKSR-2	SFPRKAS.QTSIFLQEW DIPFEQLEIG ELIGKGRFGQ
mKSR-2	SFPRKAS.QTSIFLQEW DIPFEQLEIG ELIGKGRFGQ
DmKSR	DSDRTPVRVD STEGDGSGQW RQNSISLKEW DIPYGDLLL ERIGQGRFGT
CeKSR	STIRGPN. A QASWNEVTIQ FETIEFDKQA PIIGRGRFGK

CA5

701	750
hKSR-1 (full)	VHRGRWHGEV AIRLLEMD.G HNQDH.LKLF KKEVMNYRQT RHEVVLFMG
mKSR-1	VHRGRWHGEV AIRLLEMD.G HNQDH.LKLF KKEVMNYRQT RHEVVLFMG
hKSR-1 (partial)	VHRGRWHGEV AIRLLEMD.G HNQDH.LKLF KKEVMNYRQT RHEVVLFMG
hKSR-2	YHGRWHGEV AIRLIDIE.R DNEDQ.LKAF KREVMAYRQT RHEVVLFMG
mKSR-2	YHGRWHGEV AIRLIDIE.R DNEDQ.LKAF KREVMAYRQT RHEVVLFMG
DmKSR	VHRLWHGDV AVKLLNEDYL QDEHM.LETF RSEVANFKNT RHENLVLFMG
CeKSR	VLRGFHYGDV AVKVYTMEHI SDASKKAEF KLEVSAYKNT RHDNIALFLG

CA5

751	800
hKSR-1 (full)	ACMNPPHLAI ITSFCKG.RT LHSFVRDPKT SLDINKTRQI AQEIIKGMY
mKSR-1	ACMNPPHLAI ITSFCKG.RT LHSFVRDPKT SLDINKTRQI AQEIIKGMY
hKSR-1 (partial)	ACMNPPHLAI ITSFCKG.RT LHSFVRDPKT SLDINKTRQI AQEIIKGMY
hKSR-2	ACMSPPHLAI ITSLCKG.RT LYSVVRDAKI VLDVNKTRQI AQEIVKGMY
mKSR-2	ACMSPPHLAI ITSLCKG.RT LYSVVRDAKI VLDVNKTRQI AQEIVKGMY
DmKSR	ACMNPPYLAI VTSLCKG.NT LYTYIHQRRE KFAMNRTLLI AQQIAQGMGY
CeKSR	YFMSDGQYGM VMSLSKGSQS LYTLLHVRE KLDLATTRKI AQQICQAVSY

CA5

	801	850
hKSR-1 (full)	LHAKGIVHKD LKSKNVFYDN GKVITDFGL FGISGVVREG RRENQLKLSH	
mKSR-1	LHAKGIVHKD LKSKNVFYDN GKVITDFGL FGISGVVREE RRENQLKLSH	
hKSR-1 (partial)	LHAKGIVHKD LKSKNVFYDN GKVITDFGL FGISGVVREG RRENQLKLSH	
hKSR-2	LHAKGILHKD LKSKNVFYDN GKVITDFGL FSISGVLQAG RREDKLRIQN	
mKSR-2	LHAKGILHKD LKSKNVFYDN GKVITDFGL FSISGVLQAG RRDDKLRIQN	
DmKSR	LHAREIIHKD LRTKNIFIEN GKVIITDFGL FSSTKLLYCD MG... LGVPH	
CeKSR	LHTKKILHKD LRSKNILLES KNKVVITDFG ILSMKRLAHP KQKSGYLTSLK	

CA5

	851	900
hKSR-1 (full)	DWLCYLAPEI VREMTPGKDE ... DQLPFSK AADVYAFGTV WYELQARDWP	
mKSR-1	DWLCYLAPEI VREMIPGRDE ... DQLPFSK AADVYAFGTV WYELQARDWP	
hKSR-1 (partial)	DWLCYLAPEI VREMTPGKDE ... DQLPFSK AADVYAFGTV WYELQARDWP	
hKSR-2	GWLCHLAPEI IRQLSPDTEE ... DKLPFSK HSDVFALGTL WYELHAREWP	
mKSR-2	GWLCHLAPEI IRQLSPDTEE ... DKLPFSK HSDVFALGTL WYELHAREWP	
DmKSR	NWLCLYLAPEL IRALQPEKPR G.. ECLEFTP YSDVYSGTV WYELICGEFT	
CeKSR	FWTNYIAPEL AMAMRTEYDE YECDDFPFSE NSDVYAFGCV WFEMLTGALP	

CA5

	901	950
hKSR-1 (full)	LKNQAAEASI WQIGSGEGMK RVLTSVSLGK EVSEILSACW AFDLQERPSF	
mKSR-1	FKHQPAEALI WQIGSGEGVRL VVLASVSLGK EVGEILSACW AFDLQERPSF	
hKSR-1 (partial)	LKNQAAEASI WQIGSGEGMK RVLTSVSLGK EVSEILSACW AFDLQERPSF	
hKSR-2	FKTQPAEAI WQMGTV..MK PNLSQIGMGK EISDILLFCW AFEQEERPTF	
mKSR-2	FKTQPAEAI WQMGTV..MK PNLSQIGMGK EISDILLFCW AFEQEERPTF	
DmKSR	FKDQPAESII WQVGRG..MK QSLANLQSGR DVKDLLMLCW TYEKEHRPQF	
CeKSR	YAGELPHQIL FAKTQG..IR PVLPNVKCTQ ELKELLVSCW NTAPQDRPTL	

CA5

	951	1000
hKSR-1 (full)	SLLMDMLEKL PK..LNRRRLS HPGHFWKSAD INSSKVVPRF ERFGLGVLES	
mKSR-1	SLLMDMLERL PK..LNRRRLS HPGHFWKSAD INSSKVMRPF ERFGLGTLES	
hKSR-1 (partial)	SLLMDMLEKL PK..LNRRRLS HPGHFWKSAE L.....	
hKSR-2	TKLMDMLEKL PK..RNRRRLS HPGHFWKSAE L.....	
mKSR-2	TKLMDMLEKL PK..RNRRRLS HPGHFWKSAE L.....	
DmKSR	ARLLSLLLEHL PKKRLARSPS HPVNLSRSAAE SVF.....	
CeKSR	TDINLKLTAL PKKPRVNRSP SFPVMMKSYE STF.....	

1001

hKSR-1 (full)	SNPKM
mKSR-1	GNPKM
hKSR-1 (partial)
hKSR-2
mKSR-2
DmKSR
CeKSR